

SEQUENCE LISTING

<110> Haldeman, Betty A.
Thayer, Edward C.
Sheppard, Paul O.

<120> ADIPOCYTE COMPLEMENT RELATED PROTEIN
ZACRP3X2

<130> 00-111D1

<150> US 10/012,605

<151> 2001-12-07

<150> US 60/254,019

<151> 2000-12-07

<160> 23

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<211> 957

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(957)

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1 5 10 15	
ctc cct ttt tgc ctg tgt caa gat gaa tac atg gag gtg agc gga aga	96
Leu Pro Phe Cys Leu Cys Gln Asp Glu Tyr Met Glu Val Ser Gly Arg	
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act aat aaa gtg gtg gca aga ata gtg caa agc cac cag cag act ggc	144
Thr Asn Lys Val Val Ala Arg Ile Val Gln Ser His Gln Gln Thr Gly	
35 40 45	
cgt agc ggc tcc agg agg gag aaa gtg aga gag cgg agc cat cct aaa	192
Arg Ser Gly Ser Arg Arg Glu Lys Val Arg Glu Arg Ser His Pro Lys	
50 55 60	
act ggg act gtg gat aat aac act tct aca gac cta aaa tcc ctg aga	240
Thr Gly Thr Val Asp Asn Asn Thr Ser Thr Asp Leu Lys Ser Leu Arg	
65 70 75 80	
cca gat gag cta ccg cac ccc gag gta gat gac cta gcc cag atc acc	288
Pro Asp Glu Leu Pro His Pro Glu Val Asp Asp Leu Ala Gln Ile Thr	
85 90 95	
aca ttc tgg ggc cag tct cca caa acc gga gga cta ccc cca gac tgc	336
Thr Phe Trp Gly Gln Ser Pro Gln Thr Gly Gly Leu Pro Pro Asp Cys	
100 105 110	
agt aag tgt tgt cat gga gac tac agc ttt cga ggc tac caa ggc ccc	384
Ser Lys Cys Cys His Gly Asp Tyr Ser Phe Arg Gly Tyr Gln Gly Pro	
115 120 125	
cct ggg cca ccg ggc cct cct ggc att cca gga aac cat gga aac aat	432
Pro Gly Pro Pro Gly Pro Pro Gly Ile Pro Gly Asn His Gly Asn Asn	
130 135 140	

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Gly Asn Asn Gly Ala Thr Gly His Glu Gly Ala Lys Gly Glu Lys Gly 160
145                               150                               155

gac aaa ggt gac ctg ggg cct cga ggg gag cgg ggg cag cat ggc ccc 528
Asp Lys Gly Asp Leu Gly Pro Arg Gly Glu Arg Gly Gln His Gly Pro 175
                               165                               170                               175

aaa gga gag aag ggc tac ccg ggg att cca cca gaa ctt cag att gca 576
Lys Gly Glu Lys Gly Tyr Pro Gly Ile Pro Pro Glu Leu Gln Ile Ala 190
                               180                               185                               190

ttc atg gct tct ctg gca acc cac ttc agc aat cag aac agt ggg att 624
Phe Met Ala Ser Leu Ala Thr His Phe Ser Asn Gln Asn Ser Gly Ile 205
                               195                               200                               205

atc ttc agc agt gtt gag acc aac att gga aac ttc ttt gat gtc atg 672
Ile Phe Ser Ser Val Glu Thr Asn Ile Gly Asn Phe Phe Asp Val Met 220
                               210                               215                               220

act ggt aga ttt ggg gcc cca gta tca ggt gtg tat ttc ttc acc ttc 720
Thr Gly Arg Phe Gly Ala Pro Val Ser Gly Val Tyr Phe Phe Thr Phe 240
225                               230                               235                               240

agc atg atg aag cat gag gat gtt gag gaa gtg tat gtg tac ctt atg 768
Ser Met Met Lys His Glu Asp Val Glu Glu Val Tyr Val Tyr Leu Met 255
                               245                               250                               255

cac aat ggc aac aca gtc ttc agc atg tac agc tat gaa atg aag ggc 816
His Asn Gly Asn Thr Val Phe Ser Met Tyr Ser Tyr Glu Met Lys Gly 270
                               260                               265                               270

aaa tca gat aca tcc agc aat cat gct gtg ctg aag cta gcc aaa ggg 864
Lys Ser Asp Thr Ser Ser Asn His Ala Val Leu Lys Leu Ala Lys Gly 285
                               275                               280                               285

gat gag gtt tgg ctg cga atg ggc aat ggc gct ctc cat ggg gac cac 912
Asp Glu Val Trp Leu Arg Met Gly Asn Gly Ala Leu His Gly Asp His 300
290                               295                               300                               300

caa cgc ttc tcc acc ttt gca gga ttc ctg ctc ttt gaa act aag 957
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20      25      30
Thr Asn Lys Val Val Ala Arg Ile Val Gln Ser His Gln Thr Gly
35      40      45
Arg Ser Gly Ser Arg Arg Glu Lys Val Arg Glu Arg Ser His Pro Lys
50      55      60
Thr Gly Thr Val Asp Asn Asn Thr Ser Thr Asp Leu Lys Ser Leu Arg
65      70      75      80
Pro Asp Glu Leu Pro His Pro Glu Val Asp Asp Leu Ala Gln Ile Thr
85      90      95
Thr Phe Trp Gly Gln Ser Pro Gln Thr Gly Gly Leu Pro Pro Asp Cys

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Gly	Asn	Asn	Gly	Ala	Thr	Gly	His	Glu	Gly	Ala	Lys	Gly	Glu	Lys	Gly	
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Asp	Lys	Gly	Asp	Leu	Gly	Pro	Arg	Gly	Glu	Arg	Gly	Gln	His	Gly	Pro	
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Lys	Gly	Glu	Lys	Gly	Tyr	Pro	Gly	Ile	Pro	Pro	Glu	Leu	Gln	Ile	Ala	
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Phe	Met	Ala	Ser	Leu	Ala	Thr	His	Phe	Ser	Asn	Gln	Asn	Ser	Gly	Ile	
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Ser	Met	Met	Lys	His	Glu	Asp	Val	Glu	Glu	Val	Tyr	Val	Tyr	Leu	Met	
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His	Asn	Gly	Asn	Thr	Val	Phe	Ser	Met	Tyr	Ser	Tyr	Glu	Met	Lys	Gly	
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Lys	Ser	Asp	Thr	Ser	Ser	Asn	His	Ala	Val	Leu	Lys	Leu	Ala	Lys	Gly	
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Asp	Glu	Val	Trp	Leu	Arg	Met	Gly	Asn	Gly	Ala	Leu	His	Gly	Asp	His	
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tg	aga	atc	atc	atg	ctt	tgg	agg	cag	ctc	atc	tat	tgg	caa	ctg	ctg	gct	ttg	110						
Met Leu Trp Arg Gln Leu Ile Tyr Trp Gln Leu Leu Ala Leu																								
1				5				10																
ttt	ttc	ctc	cct	ttt	tgc	ctg	tgt	caa	gat	gaa	tac	atg	gag	tct	cca	158								
Phe	Phe	Leu	Pro	Phe	Cys	Leu	Cys	Gln	Asp	Glu	Tyr	Met	Glu	Ser	Pro									
15				20				25				30												
caa	acc	gga	gga	cta	ccc	cca	gac	tgc	agt	aag	tgt	tgt	cat	gga	gac	206								
Gln	Thr	Gly	Gly	Leu	Pro	Pro	Asp	Cys	Ser	Lys	Cys	Cys	His	Gly	Asp									
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tac	agc	ttt	cga	ggc	tac	caa	ggc	ccc	cct	ggg	cca	ccg	ggc	cct	cct	254								
Tyr	Ser	Phe	Arg	Gly	Tyr	Gln	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Pro	Pro									
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ggc	att	cca	gga	aac	cat	gga	aac	aat	ggc	aac	aat	gga	gcc	act	ggt	302								
Gly	Ile	Pro	Gly	Asn	His	Gly	Asn	Asn	Gly	Asn	Asn	Gly	Ala	Thr	Gly									
65				70				75																
cat	gaa	gga	gcc	aaa	ggt	gag	aag	ggc	gac	aaa	ggt	gac	ctg	ggg	cct	350								
His	Glu	Gly	Ala	Lys	Gly	Glu	Lys	Gly	Asp	Lys	Gly	Asp	Leu	Gly	Pro									
80				85				90																
cga	ggg	gag	cgg	ggg	cag	cat	ggc	ccc	aaa	gga	gag	aag	ggc	tac	ccg	398								
Arg	Gly	Glu	Arg	Gly	Gln	His	Gly	Pro	Lys	Gly	Glu	Lys	Gly	Tyr	Pro									

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Gly Ile Pro Pro Glu Leu Gln Ile Ala Phe Met Ala Ser Leu Ala Thr	115	120	125	
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His Phe Ser Asn Gln Asn Ser Gly Ile Ile Phe Ser Ser Val Glu Thr	130	135	140	
aac att gga aac ttc ttt gat gtc atg act ggt aga ttt ggg gcc cca				542
Asn Ile Gly Asn Phe Phe Asp Val Met Thr Gly Arg Phe Gly Ala Pro	145	150	155	
gta tca ggt gtg tat ttc ttc acc ttc agc atg atg aag cat gag gat				590
Val Ser Gly Val Tyr Phe Phe Thr Phe Ser Met Met Lys His Glu Asp	160	165	170	
gtt gag gaa gtg tat gtg tac ctt atg cac aat ggc aac aca gtc ttc				638
Val Glu Glu Val Tyr Val Tyr Leu Met His Asn Gly Asn Thr Val Phe	175	180	185	190
agc atg tac agc tat gaa atg aag ggc aaa tca gat aca tcc agc aat				686
Ser Met Tyr Ser Tyr Glu Met Lys Gly Lys Ser Asp Thr Ser Ser Asn	195	200	205	
cat gct gtg ctg aag cta gcc aaa ggg gat gag gtt tgg ctg cga atg				734
His Ala Val Leu Lys Leu Ala Lys Gly Asp Glu Val Trp Leu Arg Met	210	215	220	
ggc aat ggc gct ctc cat ggg gac cac caa cgc ttc tcc acc ttt gca				782
Gly Asn Gly Ala Leu His Gly Asp His Gln Arg Phe Ser Thr Phe Ala	225	230	235	
gga ttc ctg ctc ttt gaa act aag taaatatatg actagaatag ctccactttg				836
Gly Phe Leu Leu Phe Glu Thr Lys	240	245		
gggaagactt gtagctgagc tgatttggtta cgatctgagg aacattaaag ttgagggttt				896
tacattgctg tattcaaaaa attattgggtt gcaatgttgt tcacgctaca ggtacaccaa				956
taatgttgga caattcaggg gctcagaaga atcaaccaca aaatagtctt ctcatatgac				1016
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aatgtcataa atatctcata gaggtacagt gccaatagat attcaaattg tgcattgtga				1556
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cag cag act ggc cgt agc ggc tcc agg agg gag aaa gtg aga gag cgg	96			
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agc cat cct aaa act ggg act gtg gat aat aac act tct aca gac cta	144			
Ser His Pro Lys Thr Gly Thr Val Asp Asn Asn Thr Ser Thr Asp Leu				
35 40 45				
aaa tcc ctg aga cca gat gag cta ccg cac ccc gag gta gat gac cta	192			
Lys Ser Leu Arg Pro Asp Glu Leu Pro His Pro Glu Val Asp Asp Leu				
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gag gtg agc gga aga act aat aaa gtg gtg gca aga ata gtg caa agc	96			
Glu Val Ser Gly Arg Thr Asn Lys Val Val Ala Arg Ile Val Gln Ser				
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His Gln Gln Thr Gly Arg Ser Gly Ser Arg Arg Glu Lys Val Arg Glu				
35 40 45				
cgg agc cat cct aaa act ggg act gtg gat aat aac act tct aca gac	192			
Arg Ser His Pro Lys Thr Gly Thr Val Asp Asn Asn Thr Ser Thr Asp				
50 55 60				
cta aaa tcc ctg aga cca gat gag cta ccg cac ccc gag gta gat gac	240			
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cta gcc cag atc acc aca ttc tgg ggc cag tct cca caa acc gga gga	288			
Leu Ala Gln Ile Thr Thr Phe Trp Gly Gln Ser Pro Gln Thr Gly Gly				
85 90 95				
cta ccc cca gac tgc agt aag tgt tgt cat gga gac tac agc ttt cga	336			
Leu Pro Pro Asp Cys Ser Lys Cys Cys His Gly Asp Tyr Ser Phe Arg				
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ggc tac caa ggc ccc cct ggg cca ccg ggc cct cct ggc att cca gga	384			
Gly Tyr Gln Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Ile Pro Gly				
115 120 125				
aac cat gga aac aat ggc aac aat gga gcc act ggt cat gaa gga gcc	432			
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Lys
145

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35 40 45
Leu Ser Leu Ala Leu His Leu Leu Thr Leu Cys Cys Tyr Leu Glu Leu
50 55 60
Arg Ser Glu Leu Arg Arg Glu Arg Gly Ala Glu Ser Arg Leu Gly Gly
65 70 75 80
Ser Gly Thr Pro Gly Thr Ser Gly Thr Leu Ser Ser Leu Gly Gly Leu
85 90 95
Asp Pro Asp Ser Pro Ile Thr Ser His Leu Gly Gln Pro Ser Pro Lys
100 105 110
Gln Gln Pro Leu Glu Pro Gly Glu Ala Ala Leu His Ser Asp Ser Gln
115 120 125
Asp Gly His Gln Met Ala Leu Asn Phe Phe Phe Pro Asp Glu Lys
130 135 140
Pro Tyr Ser Glu Glu Glu Ser Arg Arg Val Arg Arg Asn Lys Arg Ser
145 150 155 160
Lys Ser Asn Glu Gly Ala Asp Gly Pro Val Lys Asn Lys Lys Lys Gly
165 170 175
Lys Lys Ala Gly Pro Pro Gly Pro Asn Gly Pro Pro Gly Pro Pro Gly
180 185 190
Pro Pro Gly Pro Gln Gly Pro Pro Gly Ile Pro Gly Ile Pro Gly Ile
195 200 205
Pro Gly Thr Thr Val Met Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly
210 215 220
Pro Gln Gly Pro Pro Gly Leu Gln Gly Pro Ser Gly Ala Ala Asp Lys
225 230 235 240
Ala Gly Thr Arg Glu Asn Gln Pro Ala Val Val His Leu Gln Gly Gln
245 250 255
Gly Ser Ala Ile Gln Val Lys Asn Asp Leu Ser Gly Gly Val Leu Asn
260 265 270
Asp Trp Ser Arg Ile Thr Met Asn Pro Lys Val Phe Lys Leu His Pro
275 280 285
Arg Ser Gly Glu Leu Glu Val Leu Val Asp Gly Thr Tyr Phe Ile Tyr
290 295 300
Ser Gln Val Glu Val Tyr Tyr Ile Asn Phe Thr Asp Phe Ala Ser Tyr
305 310 315 320
Glu Val Val Val Asp Glu Lys Pro Phe Leu Gln Cys Thr Arg Ser Ile
325 330 335
Glu Thr Gly Lys Thr Asn Tyr Asn Thr Cys Tyr Thr Ala Gly Val Cys
340 345 350
Leu Leu Lys Ala Arg Gln Lys Ile Ala Val Lys Met Val His Ala Asp
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Leu Gly Glu Ala Pro Ala Ser
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<210> 7
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<213> Artificial Sequence

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gtncarwsnc aycarcacar nggnmgnwsn ggnwsnmgnm gngaraargt nmngngarmgn 180
wsncayccna aracnggnac ngtngayaay aayacnwsna cngayytnaa rwsnytnmgn 240
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carwsnccnc aracngggng nytnccnccn gaytgywsna artgytgyca yggngaytay 360
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cayggnaaya ayggnaayaa yggngcnaacn ggncaygarg gngcnaargg ngaraarggn 480
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ttygaygtna tgacnggnmg nttyggngcn ccngtnwsng gngtntaytt yttyacntty 720
wsnatgatga arcaygarga ygtngargar gtntaygtnt ayytnatgca yaayggnaay 780
acngtnttyw snatgtayws ntaygaratg aarggnaarw sngayacnws nwsnaaycay 840
gcngtnytna arytngcnaa rggngaygar gtntggytnm gnatgggnaa yggngcnnytn 900
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<221> VARIANT
<222> (7)...(7)
<223> Each Xaa is asparagine or aspartic acid

<221> VARIANT
<222> (8)...(11)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
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<223> Xaa is phenylalanine, tyrosine, tryptophan or
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<221> VARIANT
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 <223> Xaa is any amino acid residue

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 Xaa Xaa Phe Xaa Xaa Xaa Xaa Gly Xaa Tyr Xaa Phe Xaa Xaa
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<223> Oligonucleotide primer ZC38,825

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